

FASTA searches a protein or DNA sequence data bank  
version 3.3t05 March 30, 2000

Please cite:

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

/tmp/fastaCAaygaWej: 995 aa  
>SEQ ID NO:2  
vs /tmp/fastaDAazgaWej library  
searching /tmp/fastaDAazgaWej library

1008 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2  
join: 39, opt: 27, gap-pen: -12/ -2, width: 16  
Scan time: 0.034

The best scores are:

M13699 ACCESSION:M13699 NID: gi 180255 gb M13699. (1008) 2671

>>M13699 ACCESSION:M13699 NID: gi 180255 gb M13699.1 HUM (1008 aa)

initn: 1414 initl: 972 opt: 2671

Smith-Waterman score: 3980; 57.002% identity in 1014 aa overlap (1-992:1-1008)

```

      10      20      30      40      50
SEQ   MKILILGIFLFLCSPGWAIDRHCIYIGIEESIWNYPSPGKNMLNEKPFSEDL-----FLQ
      .....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
M13699 MKILILGIFLFLCSTPAWAKEKHYYIGIIEETTWDYA---SDHGEKKLISVDTEHSNIYQLQ
      10      20      30      40      50
      60      70      80      90     100     110
SEQ   GGQARKSFVFKKALYFQYTDNTFQRIIEKPSWLGFLGPMIKAETGDFIYVHVKNNASRAY
      :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :. :.
M13699 NGPDRIGRLYKKALYLQYTDFTTIEKPVWLGFLGPIIKAETGDKVYVHLKKNLASRPY
      60      70      80      90     100     110
      120     130     140     150     160     170
SEQ   SYHPHGLTYSKENEAHGAIYPDNTTGLQKEVEYLEPGKQYTYKWYVEEHQGPNDNSNCV
      ...:.....:.....:.....:.....:.....:.....:.....:.....:.....:
M13699 TFHSHGITYYKEHE--GAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNVCV
      120     130     140     150     160     170
      180     190     200     210     220     230
SEQ   TRIYHSHIDTARDVASGLIGPILTKRGTLNGDTEKDIDRSSFLMFSTTDESRSWYSDEN
      .....:.....:.....:.....:.....:.....:.....:.....:.....:
M13699 TRIYHSHIDAPKDIASGLIGPLIICKKDSLDKEKEKHIDREFVVMFSVVDENFSWYLEDN
      180     190     200     210     220     230
      240     250     260     270     280     290
SEQ   IRAF-TESGKINTSDPRFEESMSMQSINGYIYGNLPNLTMC AEDRVQWYFVGMGGVADIH
      ....:..:.....:.....:.....:.....:.....:.....:.....:.....:
M13699 IKTYCSEPEKVDKDNEFQESNRMYSVNGYTFGSLPGLSMCAEDRVKWYLFMGNEVDVH
      240     250     260     270     280     290
      300     310     320     330     340     350
SEQ   PVYLRGQTLISRNHRKDTIMLFPSSEDAFMVAKAPGVWMLGCQ----IHESMQAFFKVS
      .....:.....:.....:.....:.....:.....:.....:.....:.....:
M13699 AAFHHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQ
      300     310     320     330     340     350
```

	360	370	380	390	400	410
SEQ	NCQKPST	EAFVTGTHVIHYYIAAKEILWNYAPSGIDFFTKKNLTAAGSKSQLFFERSPTR				
M13699	ECNKSSSKDNIRGKHVRHYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFQEQTTR					
	360	370	380	390	400	410
	420	430	440	450	460	
SEQ	IGGTYKKLIYREYTDASFQTQKAR---	EEHLGILGPVFKAEV	QGTIKITFYNNASLPLSI			
M13699	IGGSYKKLVYREYTDASF	TNRKERGP	EEHLGILGPVIWAEV	GD	TIRVTFH	NKGAYPLSI
	420	430	440	450	460	470
	470	480	490	500	510	520
SEQ	QPPGLHYNKSNEGLFYE---	TPGG-STPPSSHVSPGTT	FVYTWEV	PKDVGPTSTDPNCL		
M13699	EPIGVRFNKNNEGTYYS	PNYNPQSRV	PPSASHVAPTETFTYEW	TV	PK	EVGPTNADPVCL
	480	490	500	510	520	530
	530	540	550	560	570	580
SEQ	TWFYYSSVNGK	KDINSGLLGPLLICR	NGSLGDDGKQKGV	DKEFYLLATIFDENESNLLDE		
M13699	AKMYYS	AVDPTKDIFTGLIGPMKICKK	GS	LHANGRQKD	VDKEFYLFPTVF	DENESLLED
	540	550	560	570	580	590
	590	600	610	620	630	640
SEQ	N-RTFITEPENIDKEDTDCQAS	NKMY	SINGMYGNLPGLD	TCLGDNVLWHV	FSVG	SVEDL
M13699	NIRMF	TTAPDQVDKEDE	FQES	NKMHSMNGFMYGN	QPLTMCKGDS	VVWYLF
	600	610	620	630	640	650
	650	660	670	680	690	700
SEQ	HGIYFSGNTFTSLGARRDTIP	MF	PYTSQTL	LMTPDSIGTFDLV	CMTIKHNLGGMK	KHYHV
M13699	HGIYFSGNTYLWRGER	RD	TANLFPQ	TS	LT	LHMWPDTEGTFNVECLTTDHYTGGMKQKYTV
	660	670	680	690	700	710
	710	720	730	740	750	760
SEQ	RQCGKPNPDQTQYQEEKIIITIAA	EMEWDYSPSRK	WENELHHLRRENQ	TS	SMYVDRSGTL	
M13699	NQCR	RQSEDSTFYLGERTYY-IAAVE	VEWDYSPQREWEKELHHLQE	QNV	SN	AF
	720	730	740	750	760	770
	770	780	790	800	810	820
SEQ	LGSKYKKVLYRQYDDNTFTN	QTKRNEGEK	HL	DILGPLILLNP	GQIIQIIFKNKA	ARPYSI
M13699	IGSKYKKVYRQY	TDSTFRVP	VERKAE	EEHLGILGPQLHAD	VGD	DKV
	780	790	800	810	820	830
	830	840	850	860	870	880
SEQ	HAHG	VKTNNSTVVP	TQ	PG	EIQIYT	WQIPDR
M13699	HAHG	VQTESSTV	PTPLP	GETL	TYVWKI	PERSGAGTEDSACIPWAYYSTVDQVKDLYSGLI
	840	850	860	870	880	890

```

      890      900      910      920      930
SEQ    GPLSVCR----KDINPN-IVHRVLHFMIFDENESWYFEDSINTYASKPNKVVDKENDNFQL
      ::: ::: : ::: . . . : : : : : : : : : : : : : : : : : : : : : : : : :
M13699 GPLIVCRRPYLKVFNP RRKLEFALLFLVFDENESWYLDDNIKTYS DHPEKVNKDDEEFIE
      900      910      920      930      940      950

      940      950      960      970      980      990
SEQ    SNQMHAINGRLFGNNQGITFHVGDVVNWYLGIGNEADLHTVHFHGH SFYKHKYLI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
M13699 SNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGH SFQYKHR
      960      970      980      990      1000

```

995 residues in 1 query sequences  
 1008 residues in 1 library sequences  
 Scomplib [version 3.3t05 March 30, 2000]  
 start: Wed Sep 18 11:18:07 2002 done: Wed Sep 18 11:18:08 2002  
 Scan time: 0.034 Display time: 1.433

Function used was FASTA